FIG. 1

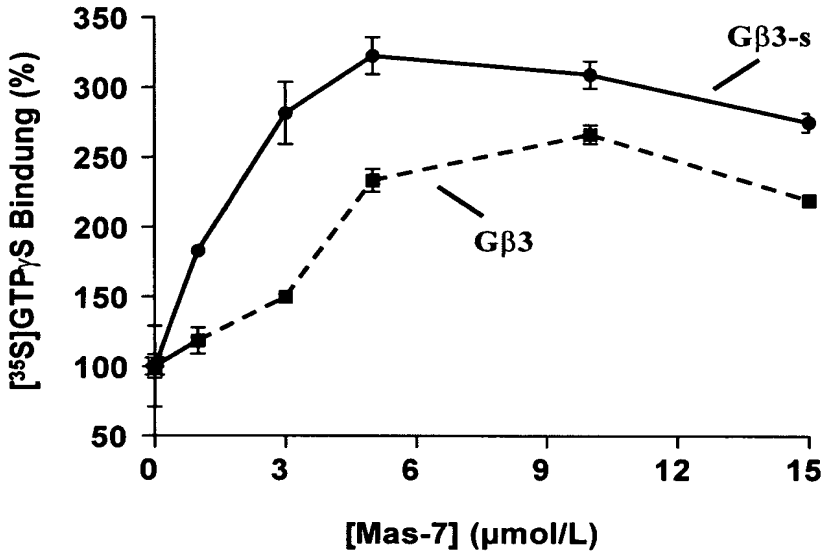

FIG. 2

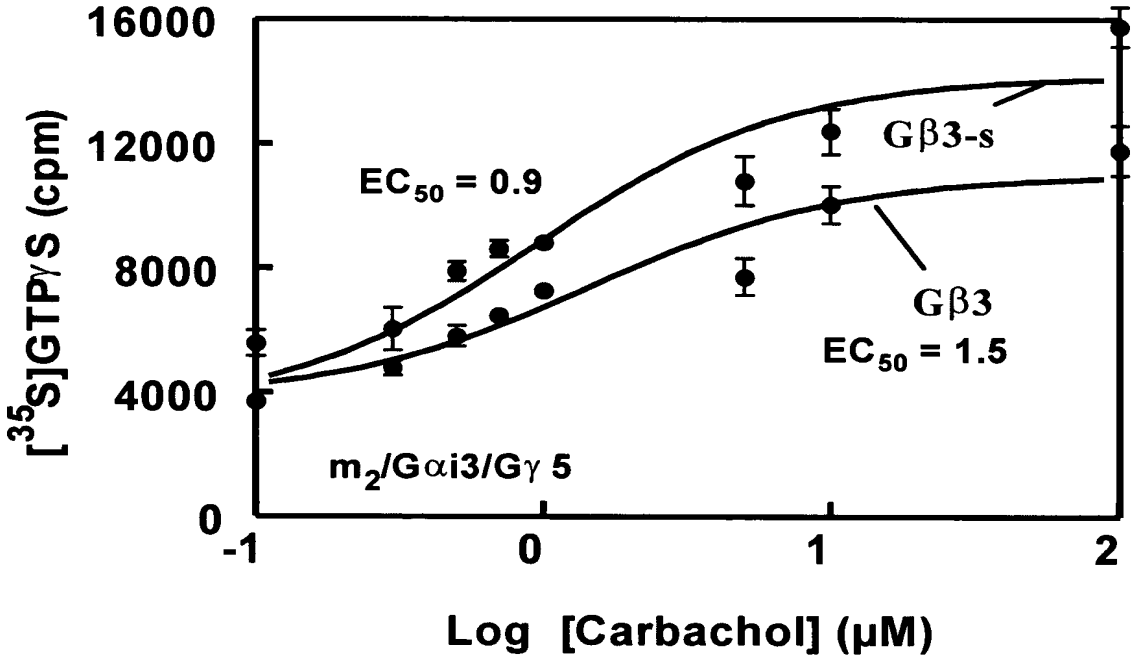

FIG. 3

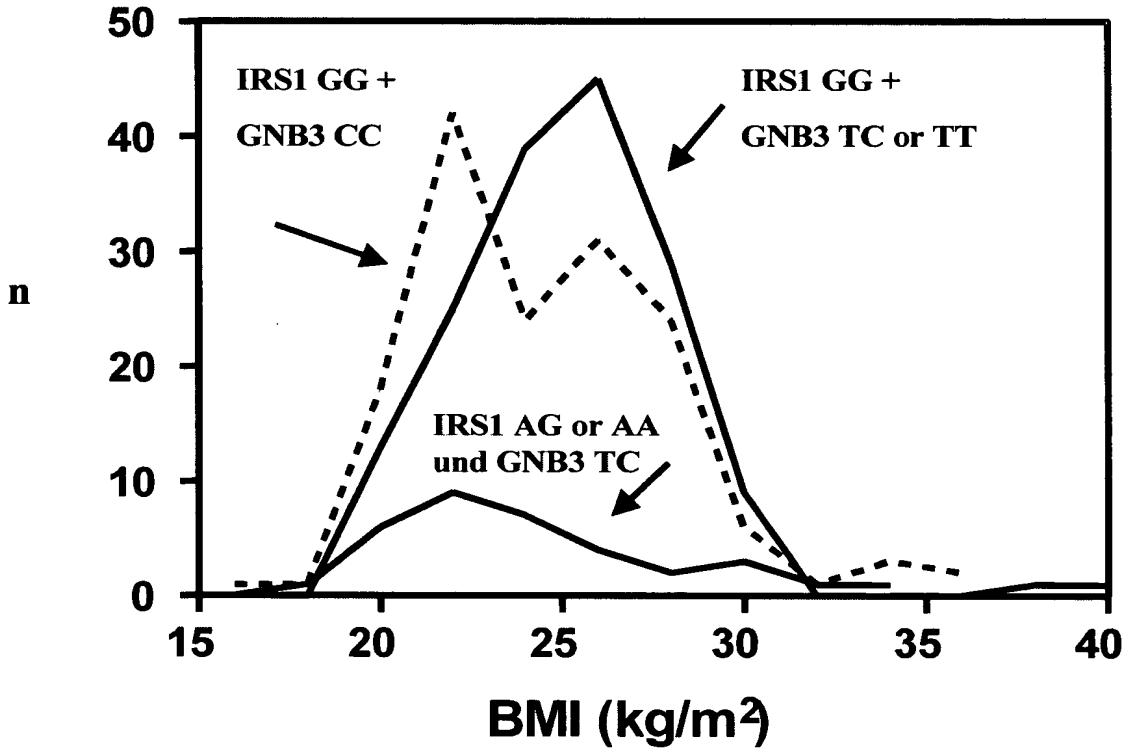

FIG. 4

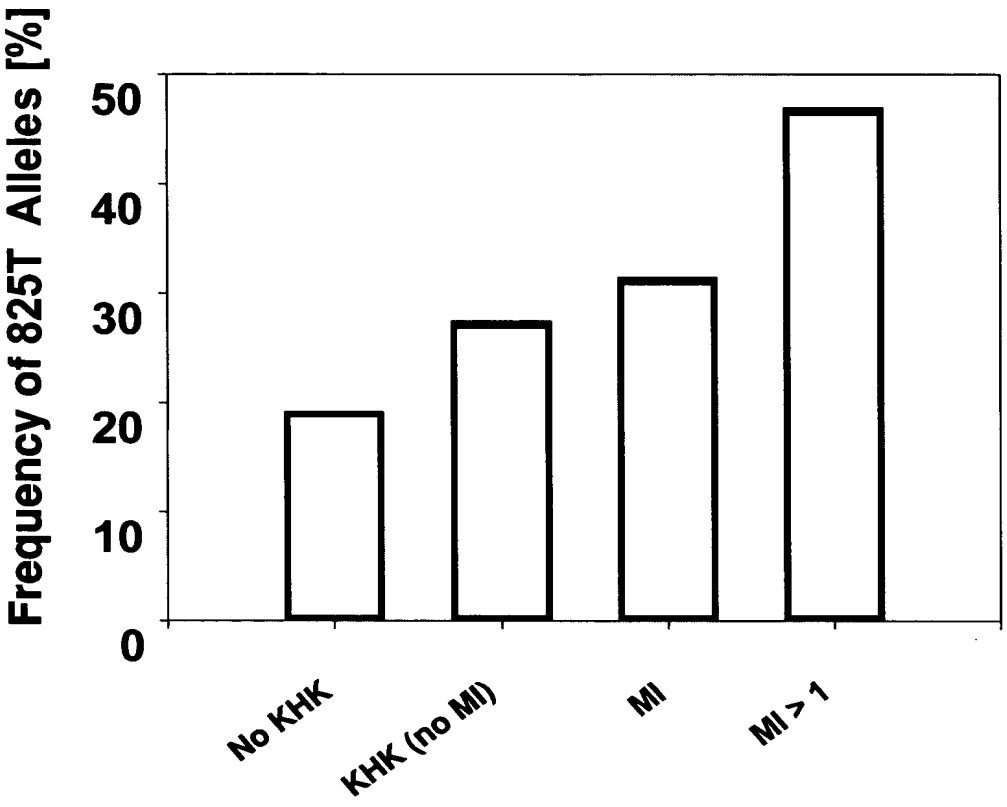

FIG. 5

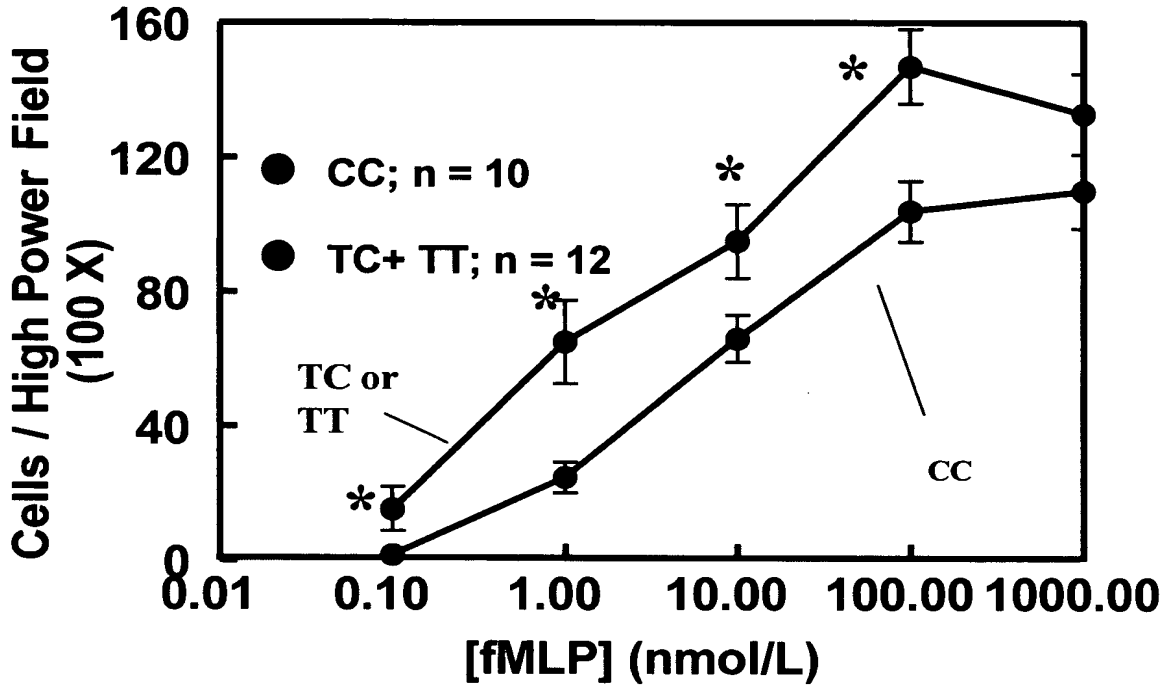

FIG. 6

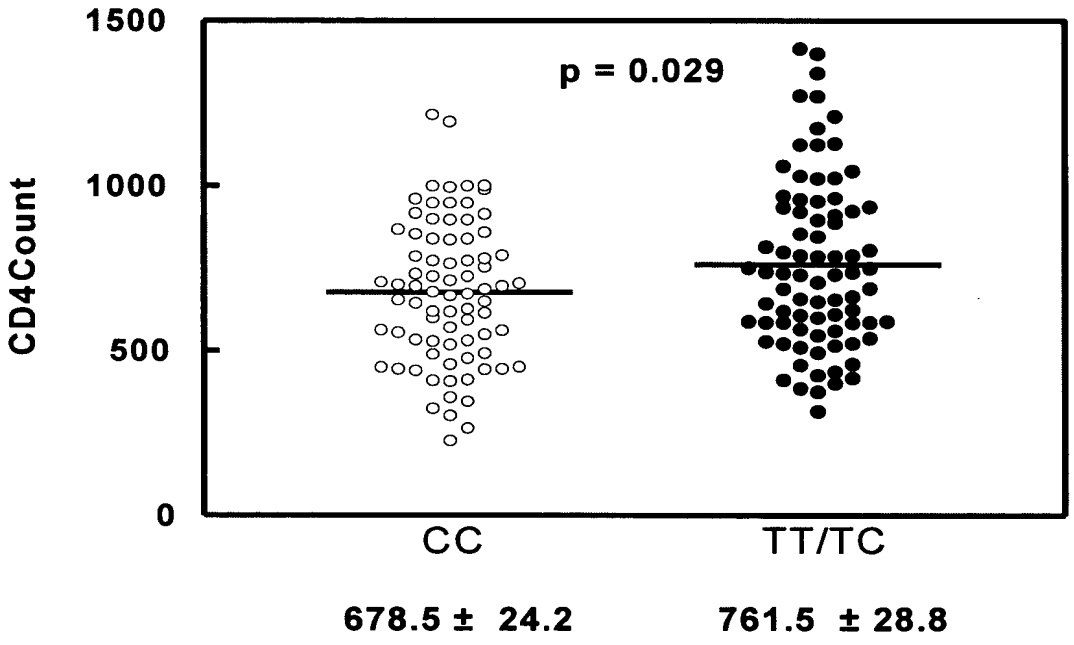

FIG. 7

Enhanced Chemotaxis of T-Lymphocytes from 825T Allele Carriers

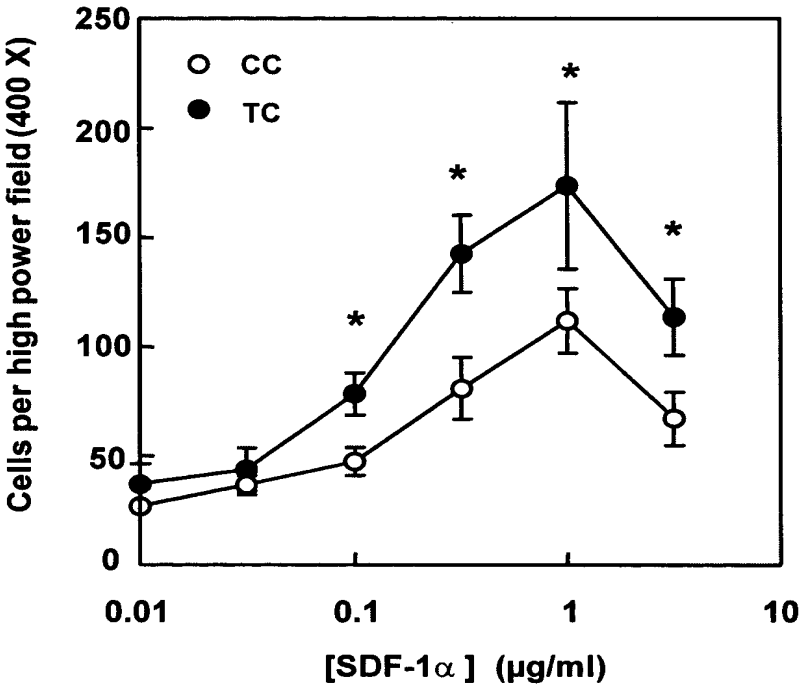

FIG. 8

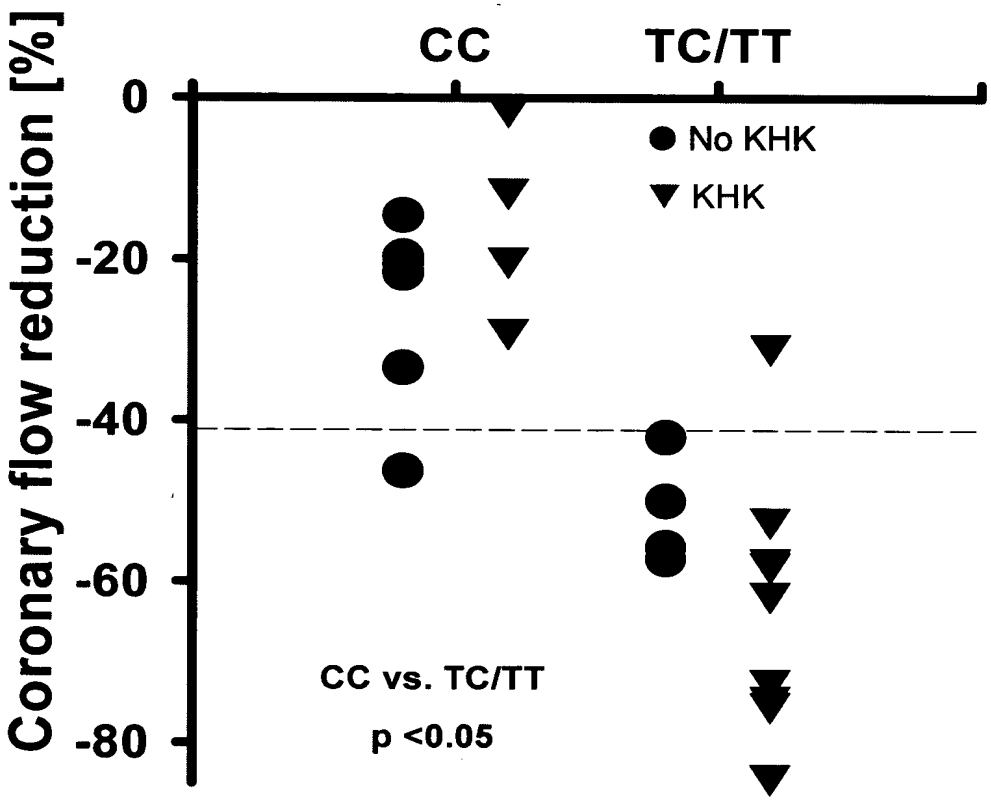

FIG. 9

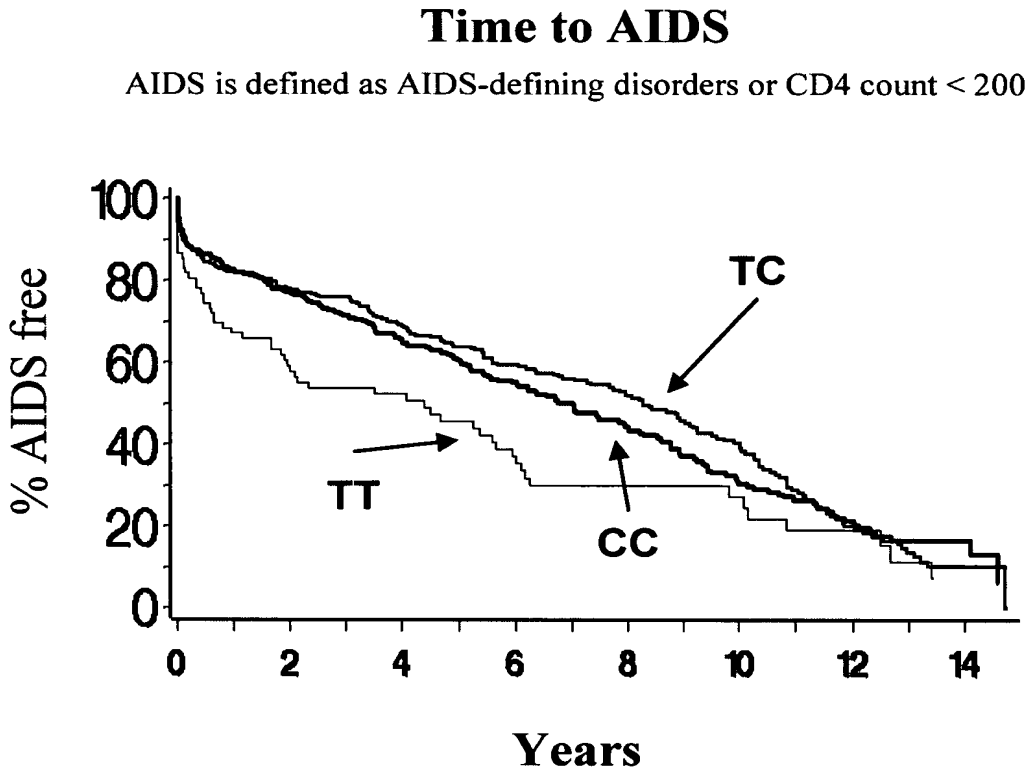

FIG. 10

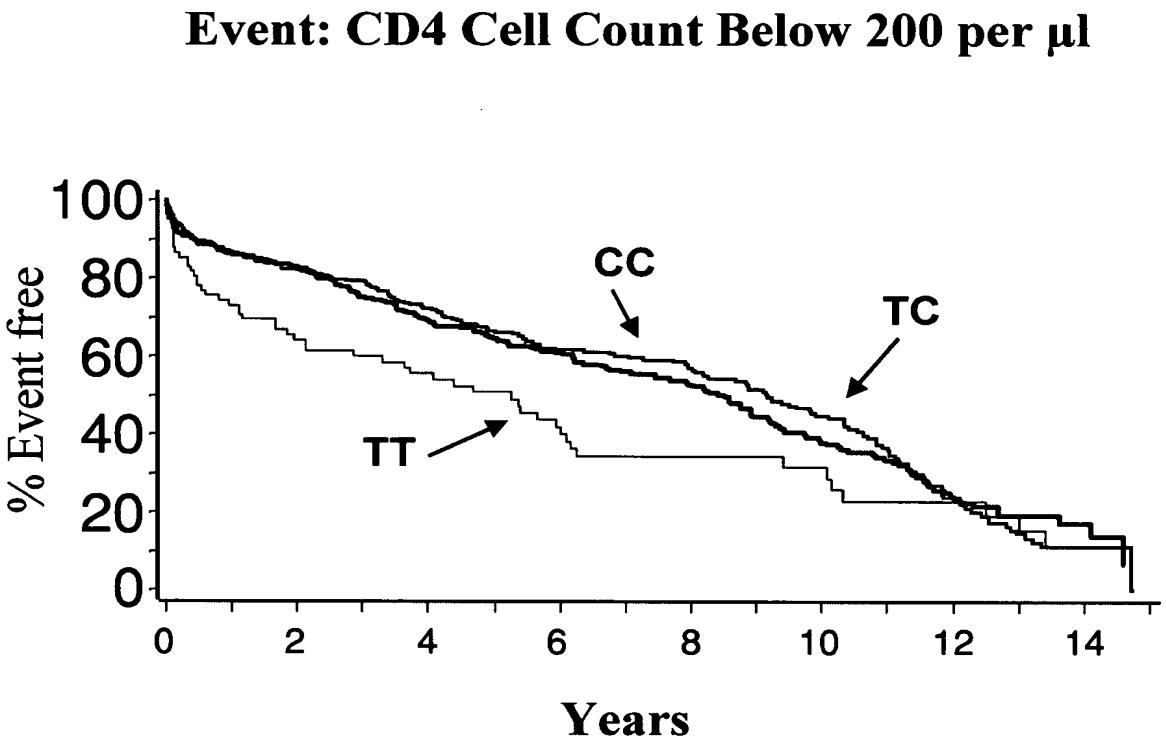

FIG. 11

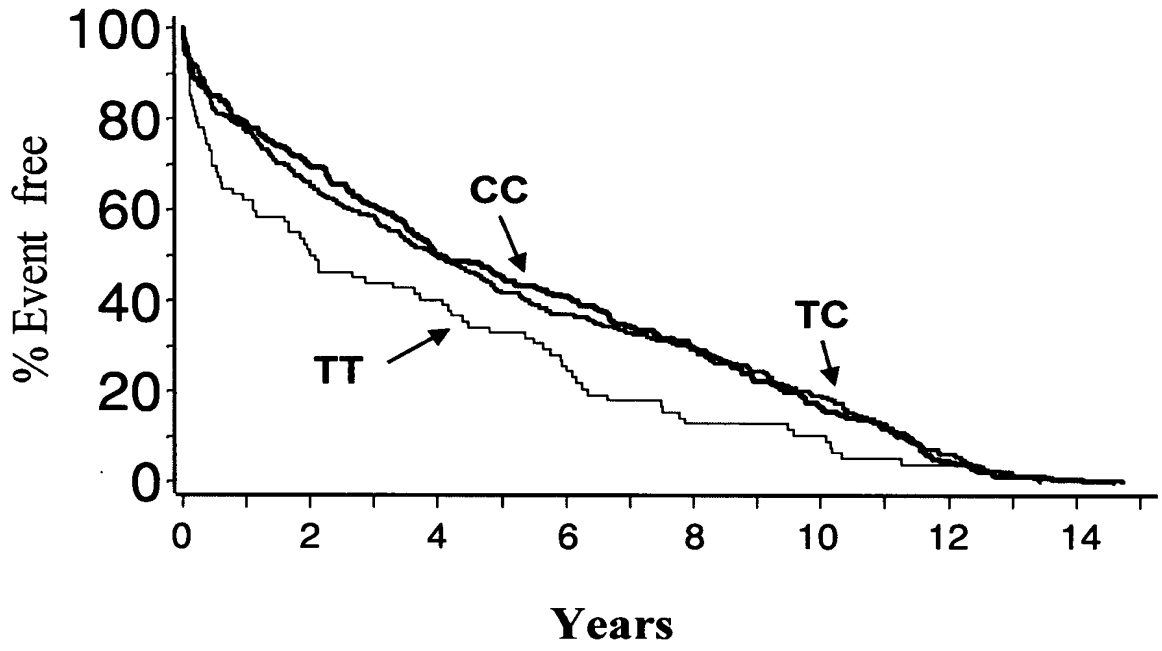

FIG. 12

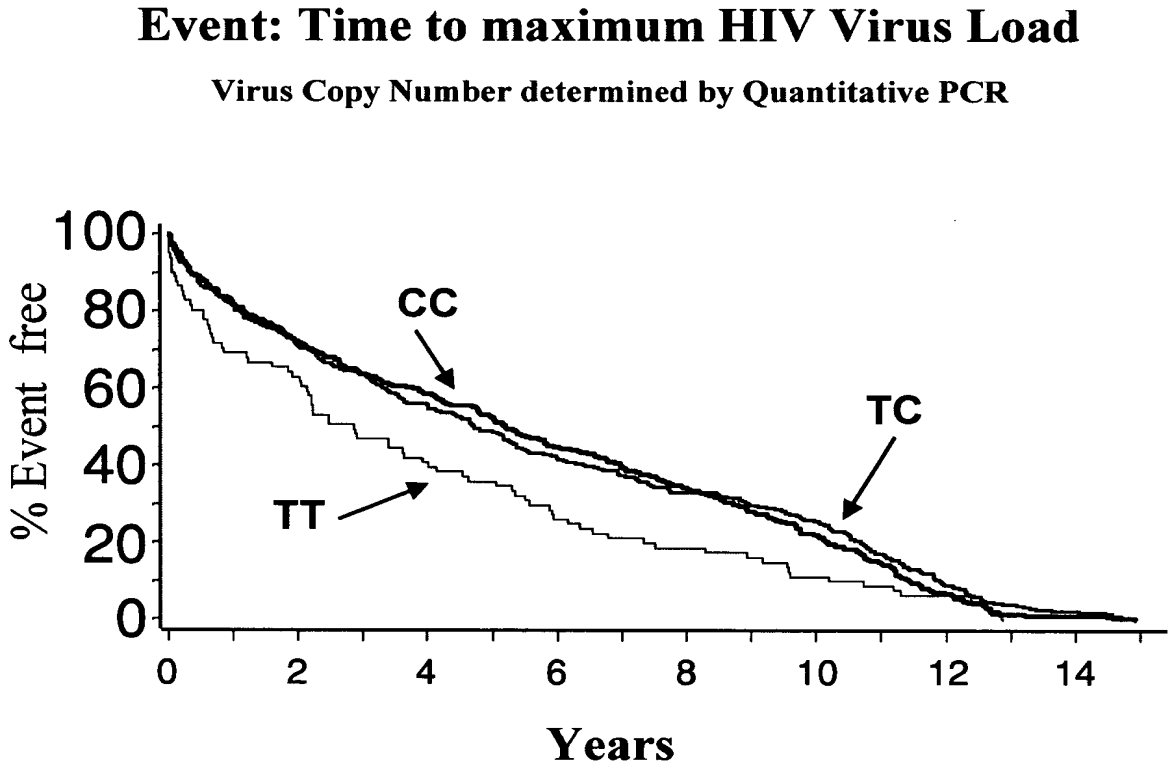

FIG. 13

FIG. 14

Potential Structures of Gβ3 and Gβ3s / Gβ3s-2

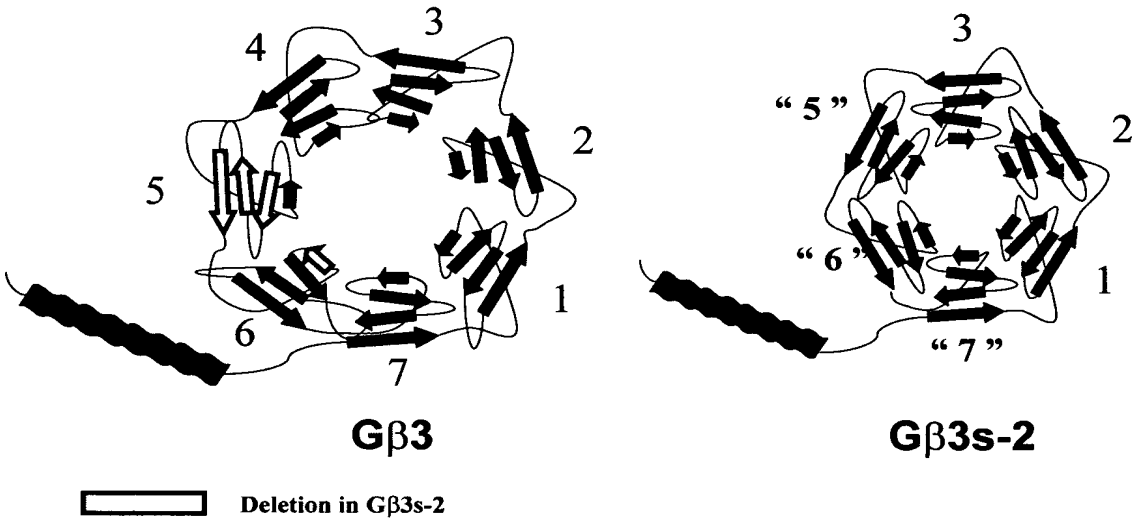

FIG. 15

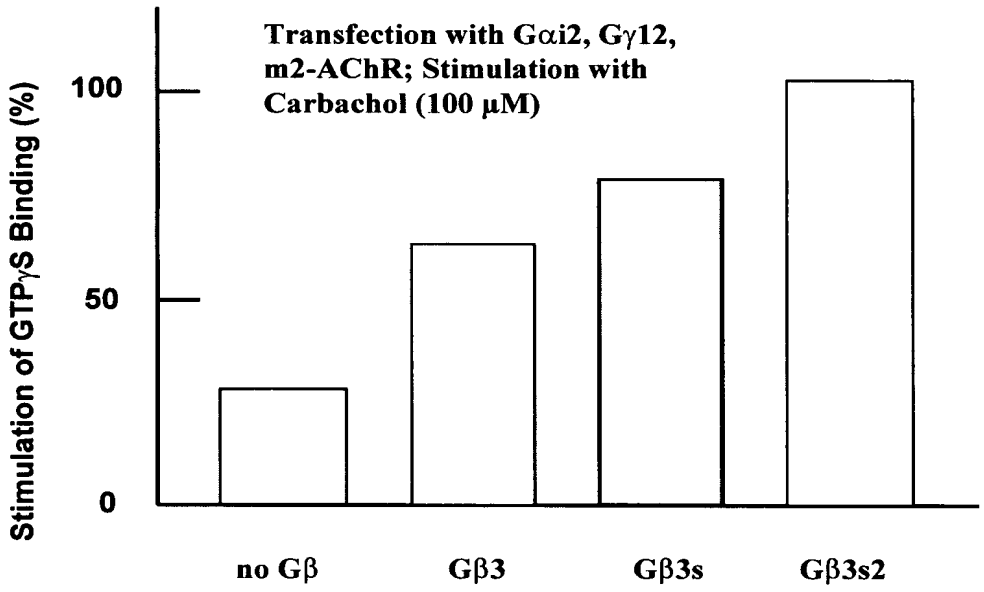

FIG. 16

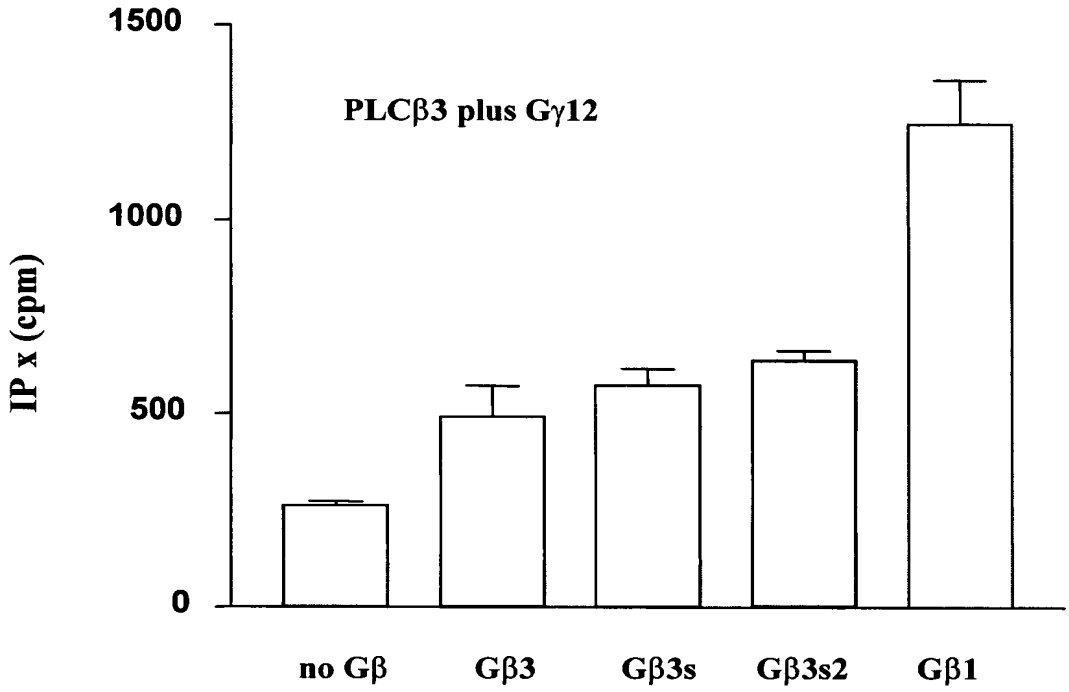

FIG. 17

ß3-original sequence of Levine. The exons are underlined alternately. The area which is omitted by cryptic splice as bold-faced.

1 gggtcg**ATGG** GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT
Start-ATG EXON 3 after Ansari-Lari
Nucleotide 1-6 seem not to be affected

61 GCAGATGCCA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTC TGGCCTAGAG
/Beginning EXON 4 /EXON 5 Beginning
==> ENDE 1 KLON ANSARI

121 GTGGTGGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT
EXON 5

181 TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG
EXON 5 / Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCACT GCGCTCCTCC
EXON 6 / EXON 7

301 TGGGTCATGA CCTGTGCCTA TGCCCCATCA GGGAACTTTG TGGCATGTGG GGGGCTGGAC
EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGGAG
EXON 7

421 CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG
EXON 7 /EXON 8

481 ACCAGCTCGG GGGACACCAC GTG**TGCCTTG TGGGACATTG AGACTGGGCA GCAGAAGACT**
EXON 8 /EXON 9
cryptic SPLICING

541 GTATTTGTGG GACACACGGG TGACTGCATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC
EXON 9
cryptic SPLICING

601 TTCATTTCGG GGGCCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC
EXON 9
cryptic **SPLICING** /

661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTTCTT CCCCAATGGA
EXON 9 / Beginning EXON 10

721 GAGGCCATCT GCACGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC
EXON 10

FIG. 17(cont.)

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCACGTC CGTGGCCTTC
EXON 10 Polymorphism site acgtc tgt

841 TCCCTCAGTG GCCGCCTACT ATTCGCTGGC TACGACGACT TCAACTGCAA TGTCTGGGAC
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGGCCACG ATAACAGGGT GAGCTGCCTG
EXON 10 /Beginning EXON 11

961 GGAGTCACAG CTGACGGGAT GGCTGTGGCC ACAGGTTCCT GGGACAGCTT CCTCAAAATC
EXON 11

1021 TGGAACTGAg gaggctggag aaagggaagt ggaaggcagt gaacacactc agcagccccc
EXON 11
End of Open Reading Frame

1081 tgcccgaccc catctcattc aggtgttctc ttctatattc cgggtgccat tcccactaag
EXON 11

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg
EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccca cagtcctcac
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agcccttgc aggcccagca
EXON 11

1321 gacttgagtc tgaggcccca ggccctagga ttcctccccc agagccacta cctttgtcca
EXON 11

"Ban Polymorphismus"
tctggcactta cta

1381 ggcctgggtg gtatagggcg tttggccctg tgactatggc tctggcacca ctagggtcct
EXON 11

1441 ggccctcttc ttattcatgc tttctccttt ttctaccttt ttttctctcc taagacacct
EXON 11

1501 gcaataaagt gtagcaccct ggt
EXON 11 POLY A SITE

FIG. 18

Sequence with two polymorphisms (Numbering after the Levine sequence)

gggtcgatgg	gggagatgga	gcaactgcgt	caggaagcgg	agcagctcaa	gaagcagatt	60
gcagatgcca	ggaaagcctg	tgctgacgtt	actctggcag	agctggtgtc	tggcctagag	120
gtggtgggac	gagtccagat	cggacgcgg	cggacgttaa	ggggacacct	ggccaagatt	180
tacgccatgc	actgggccac	tgattctaag	ctgctggtaa	gtgcctgca	agatgggaag	240
ctgatcgtgt	gggacagcta	caccaccaac	aaggtgcacg	ccatcccact	gcgctcctcc	300
tgggtcatga	cctgtgccta	tgcccatca	gggaactttg	tggcatgtgg	ggggctggac	360
aacatgtgtt	ccatctacaa	cctcaaatcc	cgtgagggca	atgtcaaggt	cagccgggag	420
ctttctgctc	acacaggtta	tctctcctgc	tgccgcttcc	tggatgacaa	caatattgtg	480
accagctcgg	gggacaccac	gtgtgccttg	tgggacattg	agactgggca	gcagaagact	540
gtatttgtgg	gacacacggg	tgactgcatg	agcctggctg	tgtctcctga	cttcaatctc	600
ttcatttcgg	gggcctgtga	tgccagtgcc	aagctctggg	atgtgcgaga	ggggacctgc	660
cgtcagactt	tcactggcca	cgagtcggac	atcaacgcca	tctgtttctt	ccccaatgga	720
gaggccatct	gcacgggctc	ggatgacgct	tcctgccgct	tgtttgacct	gcgggcagac	780
caggagctga	tctgcttctc	ccacgagagc	atcatctgcg	gcatcacgtc	ttgtggcttc	840
tccctcagtg	gccgcctact	attcgctggc	tacgacgact	tcaactgcaa	tgtctgggac	900
tccatgaagt	ctgagcgtgt	gggcatcctc	tctggccacg	ataacagggt	gagctgcctg	960
ggagtcacag	ctgacgggat	ggctgtggcc	acaggttcct	gggacagctt	cctcaaaatc	1020
tggaactgag	gaggctggag	aaagggaagt	ggaaggcagt	gaacacactc	agcagccccc	1080
tgccgaccc	catctcattc	aggtgttctc	ttctatattc	cgggtgccat	tcccactaag	1140
ctttctcctt	tgagggcagt	ggggagcatg	ggactgtgcc	tttgggaggc	agcatcaggg	1200
acacaggggc	aaagaactgc	cccatctcct	cccatggcct	tccctcccca	cagtcctcac	1260
agcctctccc	ttaatgagca	aggacaacct	gcccctcccc	agcctttgc	aggccagca	1320
gacttgagtc	tgaggcccca	ggcctagga	ttcctccccc	agagccacta	cctttgtcca	1380
tctggcacta	ctaggcctgg	gtggtatagg	gcgtttggcc	ctgtgactat	ggctctggca	1440
ccactagggt	cctggccctc	ttcttattca	tgctttctcc	ttttctacc	ttttttctc	1500
tcctaagaca	cctgcaataa	agtgtagcac	cctggt			1536

FIG. 19

Nucleic acid sequence of cDNA of Gß3 and description of the deletion in Gß3 and Gß3s-2. Numbering referenced to the cDNA of Levine et al.(Levine, M.A., Smallwood, P.M., Moen, P.T.,Jr., Helman, L.J., and Ahn, T.G. Molecular cloning of ß3 subunit, a third form of the G protein beta-subunit polypeptide. *Proc.Natl.Acad.Sci.USA* 87(6):2329-2333, 1990) Here numbering does not begin with start codon ATG, but 6 nucleotides earlier in the 5' area.

1 gggtcg**ATGG** GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT
Start-ATG EXON 3
Nucleotide 1-6 seem not to be affected

61 GCAGATGCCA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTC TGGCCTAGAG
/Beginn EXON 4 /EXON 5 Beginning

121 GTGGTGGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT
EXON 5

181 TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG
EXON 5 / Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCACT GCGCTCCTCC
EXON 6 / EXON 7

301 TGGGTCATGA CCTGTGCCTA TGCCCCATCA GGGAACTTTG TGGCATGTGG GGGGCTGGAC
EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGGAG
EXON 7

421 CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG
EXON 7 /EXON 8

Deletion bei Gß3s

481 ACCAGCTCGG GGGACACCAC GTG**TGCCTTG TGGGACATTG AGACTGGGCA GCAGAAGACT**
EXON 8 /EXON 9

541 GTATTTGTGG GACACACGGG TGACTGCATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC
EXON 9

601 TTCATTTCGG GGGCCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC
EXON 9

Deletion in Gß3s2

661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTTCTT CCCCAATGGA
EXON 9 / Beginn EXON 10
Intron dazwischen 1607 bp

FIG. 19(cont.)

Deletion in Gβ3s2

721 GAGGCCATCT GCACGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC
EXON 10

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCACGTC CGTGGCCTTC
EXON 10 polymorphism site agtc tgt

841 TCCCTCAGTG GCCGCCTACT ATTCGCTGGC TACGACGACT TCAACTGCAA TGTCTGGGAC
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGGCCACG ATAACAGGGT GAGCTGCCTG
EXON 10 /Beginning EXON 11 (Intron dazw. 989 bp)

961 GGAGTCACAG CTGACGGGAT GGCTGTGGCC ACAGGTTCCT GGGACAGCTT CCTCAAAATC
EXON 11

1021 TGGAACTGAg gaggctggag aaagggaagt ggaaggcagt gaacacactc agcagccccc
EXON 11
End of Open Reading Frame B3-3

1081 tgcccgaccc catctcattc aggtgttctc ttctatattc cgggtgccat tcccactaag
EXON 11

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg
EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccca cagtcctcac
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agcccttttgc aggcccagca
EXON 11

1321 gacttgagtc tgaggcccca ggccctagga ttcctccccc agagccacta cctttgtcca
EXON 11

C1423T
tctggcactta cta
1381 ggcctgggtg gtatagggcg tttggccctg tgactatggc tctggcactca ctagggtcct
EXON 11

1441 ggccctcttc ttattcatgc tttctccttt ttctaccttt ttttctctcc taagacacct
EXON 11

1501 gcaataaagt gtagcaccct ggt
EXON 11 POLY A SITE

FIG. 20

Amino acid sequence of Gß3s-2 (Combined production)

```
atg ggg gag atg gag caa ctg cgt cag gaa gcg gag cag ctc aag aag   48
Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Lys
                  5                                  10          15

cag att gca gat gcc agg aaa gcc tgt gct gac gtt act ctg gca gag   96
Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu Ala Glu
            20                  25                  30

ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg acg cgg  144
Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
        35                  40                  45

cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac tgg gcc  192
Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
    50                  55                  60

act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag ctg atc  240
Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
65                  70                  75                  75

gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca ctg cgc  288
Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
                80                  85                  90

tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac ttt gtg  336
Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
            95                  100                 105

gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc aaa tcc  384
Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser
        110         115                 120

cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac aca ggt  432
Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
    125                 130                 135

tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg acc agc  480
Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
140             145                 150                 155
```

FIG. 20(cont.)

```
tcg ggg gac acc acg tgt gcc ttg tgg gac att gag act ggg cag cag  528
Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
160                 165                 170                 175

aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg gct gtg  576
Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
                180                 185                 190

tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc agt gcc  624
ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
            195                 200                 205

aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc act ggc  672
Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
        210                 215                 220

cag gag tcg gac atc aac gcc atc tgt ttc ttc tcc ctc agt ggc cgc  720
His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Ser Leu Ser Gly Arg
    225                 230                 235

cta cta ttc gct ggc tac gac gac ttc aac tgc aat gtc tgg gac tcc  768
Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser
240                 245                 250                 255

atg aag tct gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg  816
Met Lys Ser Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val
            260                 265                 270

agc tgc ctg gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc  864
Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser
        275                 280                 285

tgg gac agc ttc ctc aaa atc tgg aac tga                         894
Trp Asp Ser Phe Leu Lys Ile Trp Asn ***
    290                 295
```